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Scientific and Technical Information Center
SEARCH REQUEST FORM

Requester's Full Name: Jeffrey E. Russell Examiner #: 62785 Date: 7-13-2005
Art Unit: 1654 Phone Number: 2-0969 Serial Number: 10/666,070
Location (Bldg/Room#): REM 3D19 (Mailbox #): 3C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Anti-fibril Peptides

Inventors (please provide full names): R. Hammer, Y. Fu, J. Aucoin, T. Miller, M. McLaughlin,
R. K. McCarty

Earliest Priority Date: 9-18-2003

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search SEQ ID NO:7 (KXVXFX) in the U.S. patent application sequence database (pending, published, issued), ████████, and in the UniProt/PIRL/GenBank. Please require any hits to have 30 or fewer residues.

Thank you.



STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#)	STN _____ Dialog _____
Searcher Phone #: _____	AA Sequence (#)	Questel/Orbit _____ Lexis/Nexis _____
Searcher Location: _____	Structure (#)	Westlaw _____ WWW/Internet _____
Date Searcher Picked Up: _____	Bibliographic	In-house sequence systems
Date Completed: _____	Litigation	Commercial _____ Oligomer _____ Score/Length _____ Interference _____ SPDI _____ Encode/Transl _____ Other (specify) _____
Searcher Prep & Review Time: _____	Fulltext	
Online Time: _____	Other	

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OM protein - protein search, using sw model

Run on: June 29, 2005, 15:22:51 ; Search time 160 Seconds
(without alignments)
14.504 Million cell updates/sec

Title: US-10-666-095-7

Perfect score: 18

Sequence: 1 KXVXFX 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 811763

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: geneseqp2001s:*

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7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	15	83.3	9	4	AAM24833	Aam24833 Human MHC
2	15	83.3	9	4	AAM24724	Aam24724 Human MHC
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6	15	83.3	10	4	AAM24807	Aam24807 Human MHC
7	15	83.3	10	4	AAM24793	Aam24793 Human MHC
8	15	83.3	10	4	AAM24913	Aam24913 Human MHC
9	15	83.3	10	4	AAM24898	Aam24898 Human MHC

10	15	83.3	11	2	AAW23266	Aaw23266 Tumour ne
11	15	83.3	11	4	AAB72856	Aab72856 Human p53
12	15	83.3	13	8	ADH89766	Adh89766 Cell pene
13	15	83.3	14	3	AAY56963	Aay56963 Constitut
14	15	83.3	15	2	AAY52094	Aay52094 HIV-1 pep
15	15	83.3	15	3	AAY99252	Aay99252 HLA class
16	15	83.3	17	7	ADH48641	Adh48641 Serine hy
17	15	83.3	28	8	ADO81263	Ado81263 Protein s
18	14	77.8	5	2	AAW02330	Aaw02330 Beta-amyl
19	14	77.8	5	2	AAW45963	Aaw45963 Peptide d
20	14	77.8	5	2	AAW45965	Aaw45965 Peptide d
21	14	77.8	5	2	AAW89387	Aaw89387 Beta-amyl
22	14	77.8	5	5	ABG71030	Abg71030 Long form
23	14	77.8	5	5	ABB05176	Abb05176 Beta amyl
24	14	77.8	5	5	ABB05185	Abb05185 Beta amyl
25	14	77.8	5	8	ADJ64081	Adj64081 Human bet
26	14	77.8	5	8	ADJ64090	Adj64090 Human bet
27	14	77.8	5	8	ADQ37367	Adq37367 Beta-amyl
28	14	77.8	6	4	AAB48480	Aab48480 Antifibri
29	14	77.8	6	4	AAB48488	Aab48488 Antifibri
30	14	77.8	6	4	AAB82636	Aab82636 All-D pep
31	14	77.8	6	4	AAB82628	Aab82628 All-D pep
32	14	77.8	6	5	AAU96824	Aau96824 Amyloid t
33	14	77.8	6	5	AAU96816	Aau96816 Amyloid t
34	14	77.8	6	5	AAU11662	Aau11662 Peptide #
35	14	77.8	6	5	AAU11654	Aau11654 Peptide #
36	14	77.8	6	6	AAE35450	Aae35450 Abeta pep
37	14	77.8	6	6	AAE35443	Aae35443 Abeta pep
38	14	77.8	6	8	ADQ37275	Adq37275 Vaccine a
39	14	77.8	6	8	ADQ37267	Adq37267 Vaccine a
40	14	77.8	6	8	ADQ37319	Adq37319 Antifibri
41	14	77.8	6	8	ADQ37327	Adq37327 Antifibri
42	14	77.8	8	2	AAR36140	Aar36140 Hepatitis
43	14	77.8	8	2	AAR84489	Aar84489 Hepatitis
44	14	77.8	8	2	AAR84460	Aar84460 Hepatitis
45	14	77.8	8	4	ABR52221	Abt52221 Mutant Pe

ALIGNMENTS

RESULT 1

AAM24833

ID AAM24833 standard; peptide; 9 AA.

XX

AC AAM24833;

XX

DT 04-DEC-2001 (first entry)

XX

DE Human MHC molecule HLA-A11 binding 83P5G4 peptide #10.

XX

KW 83P5G4-related protein; prostate; testis; tissue; cancer; bladder; liver; kidney; brain; bone; ovary; breast; pancreas; colon; lung; serum; cytostatic; gene therapy; antibody therapy; ribozyme; blood; cervix; single chain monoclonal antibody; urine; uterus; rectum; stomach; human; chromosome 1q31-q32.

XX

OS Homo sapiens.
XX
PN WO200159115-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004426.
XX
PR 09-FEB-2000; 2000US-0181261P.
XX
PA (UROG-) UROGENESYS INC.
XX
PI Hubert RS, Afar DEH, Challita-Eid PM, Faris M, Levin E;
PI Mitchell SC, Jakobovits A;
XX
DR WPI; 2001-514669/56.
XX
PT An isolated 83P5G4-related protein useful as a diagnostic and/or
PT therapeutic agent in multiple cancers such as prostate, bladder and bone
PT cancer.
XX
PS Example 15; Page 82; 112pp; English.
XX
CC The polypeptide sequences represent the 83P5G4-related protein and
CC peptide fragments of the protein. 83P5G4 exhibits prostate specific
CC expression in normal adult tissue, but it is also aberrantly expressed in
CC many cancers including tumours of the prostate, testis, bladder, kidney,
CC brain, bone, cervix, uterus, ovary, breast, pancreas, stomach, rectum,
CC liver, colon and lung. The 83P5G4 polynucleotide, its related protein and
CC peptide fragments and specific PCR primers are therefore useful for
CC diagnosing and treating cancer. A vector comprising a polynucleotide
CC which encodes a single chain monoclonal antibody, that immunospecifically
CC binds to an 83P5G4-related protein, and a ribozyme capable of cleaving a
CC polynucleotide having the 83P5G4 coding sequence, are both useful in the
CC preparation of a composition for treating a patient with a cancer that
CC expresses 83P5G4. The sequences can be used in diagnostic methods to
CC monitor the level of 83P5G4 gene products in serum, blood, urine and
CC tissue and to thereby detect the presence of cancerous cells
XX
SQ Sequence 9 AA;

Query Match 83.3%; Score 15; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5
| | |
Db 3 KSVAF 7

RESULT 10
AAW23266
ID AAW23266 standard; peptide; 11 AA.
XX
AC AAW23266;
XX

DT 03-NOV-1997 (first entry)
XX
DE Tumour necrosis factor alpha inhibiting peptide.
XX
KW Tumour necrosis factor; alpha; TNF-alpha; inhibition; treatment;
KW mediation; disorder; septic shock; bacterium; virus; fungus; infection;
KW autoimmune; disease; alcohol induced hepatitis; sarcoiditis; Crohn's;
KW disseminated intravascular coagulation; graft versus host; Rawasaki's;
KW tumour; bacteria.
XX
OS Synthetic.
XX
PN US5641751-A.
XX
PD 24-JUN-1997.
XX
PF 01-MAY-1995; 95US-00432694.
XX
PR 01-MAY-1995; 95US-00432694.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Heavner GA;
XX
DR WPI; 1997-340972/31.
XX
PT Peptide inhibiting tumour necrosis factor alpha - useful for treating
PT septic shock, infections, autoimmune diseases, etc.
XX
PS Disclosure; Col 23-24; 15pp; English.
XX
CC The present peptide is a tumour necrosis factor alpha (TNF-alpha)
CC inhibitor, which can be used to treat TNF-alpha mediated disorders, e.g.
CC septic shock, bacterial, viral and fungal infections, autoimmune
CC diseases, alcohol induced hepatitis, sarcoiditis, Crohn's disease,
CC disseminated intravascular coagulation, graft versus host disease,
CC Rawasaki's disease and TNF-alpha secreting tumours. The peptide is
CC preferably given as a daily dose of 1-1000, preferably 1-10 mg/kg
XX
SQ Sequence 11 AA;

Query Match 83.3%; Score 15; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5
| | |
Db 4 KSVSF 8

Search completed: June 29, 2005, 15:42:42
Job time : 163 secs

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OM protein -- protein search, using sw model

Run on: June 29, 2005, 15:40:27 ; Search time 41 Seconds
(without alignments)
10.924 Million cell updates/sec

Title: US-10-666-095-7

Perfect score: 18

Sequence: 1 KXVXFX 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 233678

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	15	83.3	11	1	US-08-432-694-16	Sequence 16, Appl
2	15	83.3	14	3	US-09-353-332-3	Sequence 3, Appl
3	15	83.3	15	4	US-09-670-075A-3	Sequence 3, Appl
4	14	77.8	5	2	US-08-612-785B-30	Sequence 30, Appl
5	14	77.8	5	3	US-08-703-675C-43	Sequence 43, Appl
6	14	77.8	5	3	US-08-617-267C-30	Sequence 30, Appl
7	14	77.8	5	3	US-08-617-267C-39	Sequence 39, Appl
8	14	77.8	5	3	US-09-095-106A-40	Sequence 40, Appl
9	14	77.8	5	3	US-09-095-106A-42	Sequence 42, Appl
10	14	77.8	6	4	US-09-747-408-7	Sequence 7, Appl
11	14	77.8	6	4	US-09-747-408-15	Sequence 15, Appl
12	14	77.8	8	1	US-08-457-804-13	Sequence 13, Appl
13	14	77.8	8	3	US-08-444-818-623	Sequence 623, App
14	14	77.8	8	3	US-08-444-818-624	Sequence 624, App
15	14	77.8	8	4	US-08-635-886C-135	Sequence 135, App

16	14	77.8	8	4	US-08-635-886C-136	Sequence 136, App
17	14	77.8	8	4	US-08-974-690C-135	Sequence 135, App
18	14	77.8	8	4	US-08-974-690C-136	Sequence 136, App
19	14	77.8	8	4	US-08-974-685-135	Sequence 135, App
20	14	77.8	8	4	US-08-974-685-136	Sequence 136, App
21	14	77.8	10	2	US-08-537-400-11	Sequence 11, Appl
22	14	77.8	12	1	US-08-305-871A-3	Sequence 3, Appli
23	14	77.8	12	4	US-09-009-953-4	Sequence 4, Appli
24	14	77.8	12	4	US-08-788-822A-4	Sequence 4, Appli
25	14	77.8	12	4	US-09-239-043D-2496	Sequence 2496, Ap
26	14	77.8	14	1	US-08-766-014-21	Sequence 21, Appl
27	14	77.8	14	2	US-08-637-759B-214	Sequence 214, App
28	14	77.8	14	2	US-08-706-702-11	Sequence 11, Appl
29	14	77.8	14	3	US-08-706-706-11	Sequence 11, Appl
30	14	77.8	14	3	US-08-871-355A-214	Sequence 214, App
31	14	77.8	14	3	US-09-019-160-16	Sequence 16, Appl
32	14	77.8	14	3	US-09-201-945-214	Sequence 214, App
33	14	77.8	14	4	US-09-238-471-11	Sequence 11, Appl
34	14	77.8	15	1	US-07-688-748A-1	Sequence 1, Appli
35	14	77.8	15	2	US-08-400-796-14	Sequence 14, Appl
36	14	77.8	18	4	US-09-763-848-4	Sequence 4, Appli
37	14	77.8	22	4	US-09-066-330-4	Sequence 4, Appli
38	14	77.8	23	4	US-09-786-569-13	Sequence 13, Appl
39	14	77.8	23	4	US-09-786-569-14	Sequence 14, Appl
40	14	77.8	23	4	US-09-786-569-16	Sequence 16, Appl
41	14	77.8	23	4	US-09-786-569-17	Sequence 17, Appl
42	14	77.8	23	4	US-09-786-569-18	Sequence 18, Appl
43	14	77.8	23	4	US-09-786-569-19	Sequence 19, Appl
44	14	77.8	23	4	US-09-270-767-57731	Sequence 57731, A
45	14	77.8	24	4	US-09-574-779B-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-08-432-694-16
; Sequence 16, Application US/08432694
; Patent No. 5641751
; GENERAL INFORMATION:
; APPLICANT: Heavner, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 5641751ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,694
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-432-694-16

Query Match 83.3%; Score 15; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 98;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 KXVXF 5
| | |
Db 4 KSVSF 8

RESULT 4

US-08-612-785B-30

Sequence 30, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-30

Query Match 77.8%; Score 14; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5
| | |
Db 1 KLVAF 5

RESULT 8

US-09-095-106A-40

; Sequence 40, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-40

Query Match 77.8%; Score 14; DB 3; Length 5;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5
| | |
Db 1 KAVFF 5

Search completed: June 29, 2005, 15:55:13
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 15:45:43 ; Search time 156 Seconds
(without alignments)
14.790 Million cell updates/sec

Title: US-10-666-095-7

Perfect score: 18

Sequence: 1 KXVXF 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 384854

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
1	15	83.3	9	9	US-09-780-053-217	Sequence 217, App
2	15	83.3	9	9	US-09-780-053-326	Sequence 326, App
3	15	83.3	10	9	US-09-780-053-83	Sequence 83, Appl
4	15	83.3	10	9	US-09-780-053-278	Sequence 278, App
5	15	83.3	10	9	US-09-780-053-286	Sequence 286, App
6	15	83.3	10	9	US-09-780-053-300	Sequence 300, App
7	15	83.3	10	9	US-09-780-053-391	Sequence 391, App
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14	14	77.8	5	9	US-09-972-475-39	Sequence 39, Appl
15	14	77.8	5	15	US-10-463-729-30	Sequence 30, Appl
16	14	77.8	5	15	US-10-463-729-39	Sequence 39, Appl
17	14	77.8	5	16	US-10-721-774-40	Sequence 40, Appl
18	14	77.8	5	16	US-10-721-774-42	Sequence 42, Appl
19	14	77.8	6	9	US-09-867-847-16	Sequence 16, Appl
20	14	77.8	6	9	US-09-867-847-24	Sequence 24, Appl
21	14	77.8	6	9	US-09-915-092-6	Sequence 6, Appl
22	14	77.8	6	9	US-09-915-092-14	Sequence 14, Appl
23	14	77.8	6	10	US-09-747-408-7	Sequence 7, Appl
24	14	77.8	6	10	US-09-747-408-15	Sequence 15, Appl
25	14	77.8	6	17	US-10-728-028-6	Sequence 6, Appl
26	14	77.8	6	17	US-10-728-028-14	Sequence 14, Appl
27	14	77.8	6	17	US-10-825-958-14	Sequence 14, Appl
28	14	77.8	6	17	US-10-825-958-22	Sequence 22, Appl
29	14	77.8	8	15	US-10-651-165-135	Sequence 135, App
30	14	77.8	8	15	US-10-651-165-136	Sequence 136, App
31	14	77.8	8	16	US-10-182-040C-21	Sequence 21, Appl
32	14	77.8	8	16	US-10-031-123B-14	Sequence 14, Appl
33	14	77.8	8	17	US-10-808-187-1343	Sequence 1343, Ap
34	14	77.8	9	15	US-10-363-791-208	Sequence 208, App
35	14	77.8	10	10	US-09-572-270A-606	Sequence 606, App
36	14	77.8	10	10	US-09-572-270A-608	Sequence 608, App
37	14	77.8	10	10	US-09-573-822C-646	Sequence 646, App

38	14	77.8	10	15	US-10-363-791-113	Sequence 113, App
39	14	77.8	10	15	US-10-363-791-171	Sequence 171, App
40	14	77.8	10	17	US-10-808-187-551	Sequence 551, App
41	14	77.8	11	17	US-10-808-187-624	Sequence 624, App
42	14	77.8	11	17	US-10-494-175-6	Sequence 6, Appli
43	14	77.8	11	17	US-10-947-352-3	Sequence 3, Appli
44	14	77.8	12	13	US-10-103-395-4	Sequence 4, Appli
45	14	77.8	12	15	US-10-149-138-4208	Sequence 4208, Ap

ALIGNMENTS

RESULT 1

US-09-780-053-217

; Sequence 217, Application US/09780053
; Patent No. US20020102640A1
; GENERAL INFORMATION:
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Mary Faris
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 83P5G4: A TISSUE SPECIFIC PROTEIN
; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: 129.5USU1
; CURRENT APPLICATION NUMBER: US/09/780,053
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/181,261
; PRIOR FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 716
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapiens

US-09-780-053-217

Query Match 83.3%; Score 15; DB 9; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 KXVXF 5
| | |
Db 3 KSVAF 7

Search completed: June 29, 2005, 15:59:03
Job time : 157 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 15:32:26 ; Search time 38 Seconds
(without alignments)
15.192 Million cell updates/sec

Title: US-10-666-095-7

Perfect score: 18

Sequence: 1 KXVXFX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6283

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	14	77.8	17	2	B61491	seed protein ws-2
2	14	77.8	21	2	D61497	seed protein ws-19
3	14	77.8	24	2	PQ0677	photosystem I 9.0K
4	14	77.8	24	2	PQ0676	photosystem I 9.2K
5	14	77.8	24	2	C56819	PS I complex subun
6	14	77.8	26	2	B84724	hypothetical prote
7	14	77.8	29	2	I49732	NADH2 dehydrogenas
8	13	72.2	14	2	S29632	xylan 1,4-beta-xyl
9	13	72.2	16	2	S11805	heat shock protein
10	13	72.2	19	2	A61110	68K collagen-bindi
11	13	72.2	20	2	I49423	cytotoxic T-lympho
12	13	72.2	20	2	S07232	ribulose-bisphosph
13	13	72.2	20	2	PC4385	GroEL protein homo
14	13	72.2	20	2	A44921	hydroxypyruvate re
15	13	72.2	20	2	PC4386	GroEL protein homo

16	13	72.2	20	2	JU0330	hypothetical prote
17	13	72.2	20	2	A61150	2-oxoglutarate dec
18	13	72.2	20	2	A99091	hypothetical prote
19	13	72.2	22	2	A56868	heat shock protein
20	13	72.2	24	2	A40288	chaperonin 60 - Rh
21	13	72.2	28	2	B39116	epidermal growth f
22	13	72.2	30	2	B43591	45K outer membrane
23	13	72.2	30	2	A53415	lectin chain A - I
24	12	66.7	10	2	S48182	bacterioferritin -
25	12	66.7	11	2	PC2372	58K heat shock pro
26	12	66.7	11	2	YHHU	morphogenetic neur
27	12	66.7	11	2	YHBO	morphogenetic neur
28	12	66.7	11	2	YHJFHY	morphogenetic neur
29	12	66.7	11	2	YHXAE	morphogenetic neur
30	12	66.7	11	2	YHRT	morphogenetic neur
31	12	66.7	14	2	S60353	amylopullulanase -
32	12	66.7	14	2	C59137	protein Pf3 - gold
33	12	66.7	16	2	S22677	heat shock protein
34	12	66.7	16	2	S24667	protein-tyrosine k
35	12	66.7	17	2	S05930	chorion class B pr
36	12	66.7	17	2	S05922	chorion class B pr
37	12	66.7	17	2	S05936	chorion class B pr
38	12	66.7	20	2	C60894	gamma crystallin I
39	12	66.7	21	2	A36902	orfB2 - Escherichi
40	12	66.7	26	2	S26228	ribosomal protein
41	12	66.7	30	2	S15678	acetylcholinestera
42	12	66.7	30	2	B29164	cartilage proteogl
43	12	66.7	30	2	B81956	hypothetical prote
44	12	66.7	30	2	D82251	hypothetical prote
45	11	61.1	9	2	B20569	serum amyloid P-co

ALIGNMENTS

RESULT 1

B61491

seed protein ws-2 - winged bean (fragment)

C;Species: Psophocarpus tetragonolobus (winged bean)

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C;Accession: B61491

R;Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A;Title: Microsequence analysis of winged bean seed proteins electroblotted from two-dimensional gel.

A;Reference number: A61491; MUID:89351606; PMID:2765119

A;Accession: B61491

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-17 <HIR>

A;Cross-references: UNIPROT:Q7M1H7

C;Keywords: seed

Query Match 77.8%; Score 14; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 2.1e+02;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5
| : |
Db 1 KTISF 5

Search completed: June 29, 2005, 15:46:19
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 15:24:30 ; Search time 165 Seconds
(without alignments)
18.621 Million cell updates/sec

Title: US-10-666-095-7
Perfect score: 18
Sequence: 1 KXVXFX 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 26236

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
<hr/>						
1	15	83.3	20	2	Q9R497	Q9r497 vibrio chol
2	14	77.8	8	2	Q56759	Q56759 xanthobacte
3	14	77.8	14	2	Q85718	Q85718 reovirus ty
4	14	77.8	17	2	Q7M1H7	Q7m1h7 psophocarpu
5	14	77.8	19	2	Q85671	Q85671 reovirus ty
6	14	77.8	20	2	Q85670	Q85670 reovirus ty
7	14	77.8	21	2	Q7M1H8	Q7m1h8 psophocarpu
8	14	77.8	23	1	CH60 THIFE	P29134 thiobacillu

9	14	77.8	24	1	PSAH_CUCSA	P42050 cucumis sat
10	14	77.8	24	2	Q714T9	Q714t9 fragilaria
11	14	77.8	24	2	Q9T2J0	Q9t2j0 nicotiana t
12	14	77.8	24	2	Q9T2J1	Q9t2j1 nicotiana t
13	14	77.8	25	2	Q72001	Q72001 human immun
14	14	77.8	29	1	NUO1_SOLTU	P80267 solanum tub
15	14	77.8	30	2	Q8CTE8	Q8cte8 staphylococ
16	13	72.2	8	2	Q93SP2	Q93sp2 pseudomonas
17	13	72.2	13	1	CH60_CANFA	P49818 canis famil
18	13	72.2	14	2	Q9UH91	Q9uh91 homo sapien
19	13	72.2	14	2	Q7M0Q6	Q7m0q6 thermotoga
20	13	72.2	17	2	Q9S889	Q9s889 narcissus p
21	13	72.2	18	1	RL24_PROVU	P20032 proteus vul
22	13	72.2	18	1	RL24_SERMA	P49624 serratia ma
23	13	72.2	18	2	Q9R522	Q9r522 francisella
24	13	72.2	20	2	Q7RR59	Q7rr59 plasmodium
25	13	72.2	20	2	Q7M266	Q7m266 euglena gra
26	13	72.2	20	2	Q9S8P0	Q9s8p0 raphanus sa
27	13	72.2	20	2	Q49132	Q49132 methylobact
28	13	72.2	20	2	Q8CYA3	Q8cya3 streptococc
29	13	72.2	20	2	Q62546	Q62546 mus spretus
30	13	72.2	21	2	P70861	P70861 borrelia bu
31	13	72.2	22	1	CH60_BOVIN	P31081 bos taurus
32	13	72.2	22	2	Q9TLD2	Q9tld2 bostrychia
33	13	72.2	23	2	Q8MFI5	Q8mfi5 sphaerocion
34	13	72.2	23	2	Q8MFI9	Q8mfi9 hymenophyll
35	13	72.2	23	2	Q8MFJ1	Q8mfj1 hymenophyll
36	13	72.2	23	2	Q8MFJ3	Q8mfj3 hymenophyll
37	13	72.2	23	2	Q8MFJ5	Q8mfj5 hymenophyll
38	13	72.2	23	2	Q8MFJ7	Q8mfj7 hymenophyll
39	13	72.2	23	2	Q8MFJ9	Q8mfj9 hymenophyll
40	13	72.2	23	2	Q8MFK1	Q8mfk1 hymenophyll
41	13	72.2	23	2	Q8MFK3	Q8mfk3 hymenophyll
42	13	72.2	23	2	Q8MFK5	Q8mfk5 hymenophyll
43	13	72.2	23	2	Q9R590	Q9r590 neisseria m
44	13	72.2	24	1	CH60_ACICA	P81874 acinetobact
45	13	72.2	24	1	CH60_HELVI	P26317 heliothis v

ALIGNMENTS

RESULT 1

Q9R497

ID Q9R497 PRELIMINARY; PRT; 20 AA.
 AC Q9R497;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Outer membrane protein 38 kDa monomeric subunit (Fragment).
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96134988; PubMed=8550475;

RA Chakrabarti S.R., Chaudhuri K., Sen K., Das J.;
RT "Porins of *Vibrio cholerae*: purification and characterization of
RT OmpU.";
RL *J. Bacteriol.* 178:524-530(1996).
SQ SEQUENCE 20 AA; 2199 MW; CF50A18B305A5052 CRC64;

Query Match 83.3%; Score 15; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXVXF 5
| | |
Db 9 KAVSF 13

Search completed: June 29, 2005, 15:45:34
Job time : 168 secs